



Fungal Planet 1049 – 29 June 2020

## *Juncomyces* Crous, *gen. nov.*

*Etymology.* Name refers to the host genus *Juncus* from which it was isolated.

*Classification* — *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetes*.

*Mycelium* consisting of brown, smooth to warty, septate, branched. *Conidiophores* solitary, subcylindrical, mostly unbranched, erect, thick-walled, brown, verruculose, warty, multiseptate, rarely forming from a brown stroma, with a few fasciculate con-

idiophores. *Conidiogenous cells* integrated, terminal, straight to geniculate-sinuuous, proliferating sympodially with several apical loci, flattened, thickened, darkened, and refractive. *Conidia* solitary, acicular to slightly obclavate, mostly thick-walled, verruculose, guttulate, apex subobtuse, base truncate, thickened, darkened and refractive, septate.

*Type species.* *Juncomyces californiensis* Crous.  
MycBank MB835403.

## *Juncomyces californiensis* Crous, *sp. nov.*

*Etymology.* Name refers to the state of California, where it was collected.

*Mycelium* consisting of brown, smooth to warty, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, subcylindrical, mostly unbranched, erect, 80–180 × 5–7 µm, thick-walled, brown, verruculose, warty, multiseptate, rarely forming from a brown stroma, up to 120 µm diam, with 1–3 fasciculate conidiophores, up to 60 µm tall. *Conidiogenous cells* integrated, terminal, straight to geniculate-sinuuous, 35–60 × 5–7 µm; proliferating sympodially with several apical loci, flattened, thickened, darkened, and refractive, 4.5–5.5 µm diam. *Conidia* solitary, acicular to slightly obclavate, mostly thick-walled, verruculose, guttulate, apex subobtuse, base truncate, 4.5–5 µm diam, thickened, darkened and refractive, 3(–6)-septate, (65–)70–85(–90) × (7–)8(–9) µm.

*In vivo:* *Conidiophores* on culms erect, solitary, rarely in fascicles of 2–3, straight, 2–6-septate, subcylindrical, rejuvenating percurrently, 50–110 × 5–7 µm, arising from immersed, brown, weakly developed stroma, 20–40 µm diam. *Conidiogenous cells* integrated, terminal and intercalary, medium brown, smooth, 10–45 × 5–6 µm with one to several loci, round, thickened, refractive, 3–4 µm diam. *Conidia* solitary, arranged in clusters on conidiophores, obclavate, slightly curved to straight, apex subobtuse, base truncate, 3–7-septate, at times constricted at some of the septa, thick-walled, medium brown, verruculose, hilum thickened, darkened, refractive, 4–5 µm diam, (45–)55–70(–75) × (6–)7(–8) µm.

*Culture characteristics* — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, feathery, even margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

*Typus.* USA, California, UC Davis, on leaves of *Juncus effusus* (*Juncaceae*), 3 Apr. 2019, P.W. Crous, HPC 2894 (holotype CBS H-24363, culture ex-type CPC 37989 = CBS 146682; ITS and LSU sequences GenBank MT373368.1 and MT373351.1, MycoBank MB835405).

*Additional material examined.* USA, California, UC Davis, on leaves of *J. effusus*, 3 Apr. 2019, P.W. Crous, HPC 2895, culture CPC 37993 = CBS 146631; ITS, LSU and *rpb2* sequences GenBank MT373369.1, MT373352.1 and MT375101.1.

*Colour illustrations.* *Juncus effusus* growing in California. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

*Notes* — *Juncomyces* is closely related to *Graminopassalora*, which was introduced to accommodate *Passalora graminis*, a widespread pathogen occurring on a broad range of grass (*Poaceae*) hosts (Videira et al. 2017). *Juncomyces* differs from *Graminopassalora* by chiefly having solitary conidiophores (rarely fascicles of 2–3), and multiseptate, obclavate conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 37989 had highest similarity to *Graminopassalora graminis* (strain CBS 113303, GenBank GU214666.1; Identities = 474/538 (88 %), 18 gaps (3 %)), *Mycosphaerella fimbriata* (strain CBS 120736, GenBank NR\_137553.1; Identities = 465/526 (88 %), 16 gaps (3 %)), and *Zasmidium corymbiae* (strain CBS 145049, GenBank MK047423.1; Identities = 476/542 (88 %), 21 gaps (3 %)). The ITS sequences of CPC 37989 and 37993 are 100 % (528/528 bp) identical. Closest hits using the **LSU** sequence of CPC 37989 are *Xenosonderhenia eucalypti* (strain CBS 138858, GenBank NG\_058120.1; Identities = 773/799 (97 %), 2 gaps (0 %)), *Ramularia lethalis* (strain CPC 25910, GenBank KX287174.1; Identities = 780/808 (97 %), no gaps), and *Ramularia acris* (strain CBS 109794, GenBank KX287010.1; Identities = 780/808 (97 %), no gaps). The LSU sequences of CPC 37989 and 37993 are 100 % (808/808 bp) identical. Closest hits using the **rpb2** sequence of CPC 37993 had highest similarity to *Ramularia gei* (strain CBS 344.49, GenBank KX288570.1; Identities = 637/840 (76 %), 14 gaps (1 %)), *Ramularia unterseheri* (strain CBS 124884, GenBank KP894709.1; Identities = 636/849 (75 %), 8 gaps (0 %)), and *Ramularia heraclei* (strain CPC 11507, GenBank KX288584.1; Identities = 634/848 (75 %), 6 gaps (0 %)).